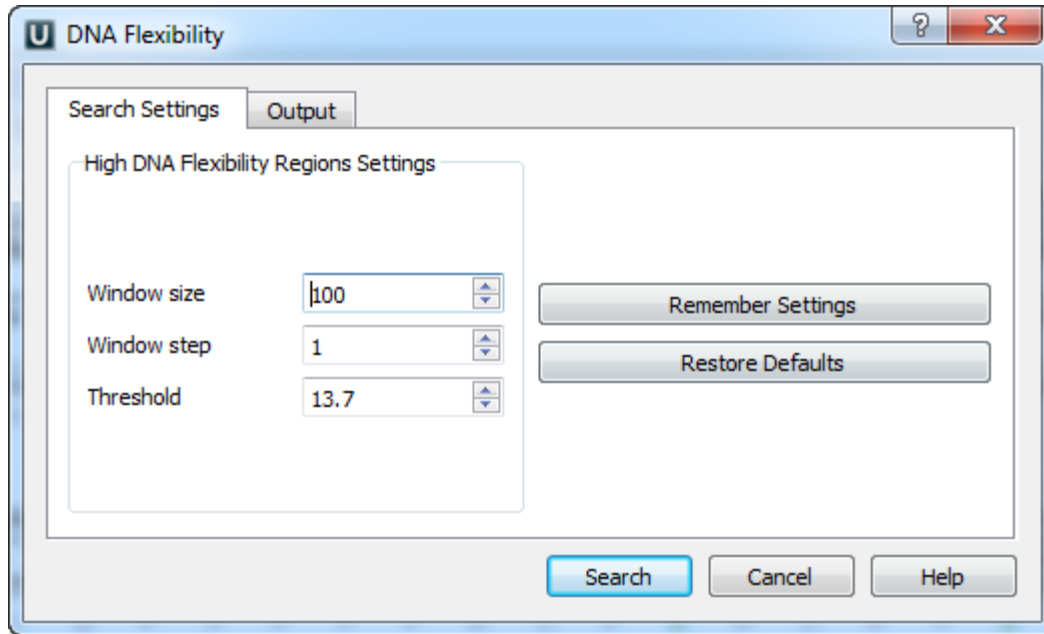


# DNA Flexibility

To search for regions of high DNA helix flexibility in a DNA sequence, open the sequence in the *Sequence View* and select the *Analyze Find high DNA flexibility regions* item in the context menu. Note that only standard DNA alphabet is supported, i.e. the sequence should consist of characters A, C, G, T and N.

The following dialog appears:



The calculation is made for overlapping windows along a given sequence. If there are two or more consecutive windows with an average flexibility threshold (in each window) greater than the specified *Threshold* parameter, such area is marked by an *annotation*.

The average threshold in a window is calculated by the following formula:

$$(\text{average window threshold}) = (\text{sum of flexibility angles in the window}) / (\text{the window size} - 1)$$

The following flexibility angles are used during the calculation:

Dinucleotide	Angle	Dinucleotide	Angle
AA	7.6	CA	14.6
AC	10.9	CC	7.2
AG	8.8	CG	11.1
AT	12.5	CT	8.8
GA	8.2	TA	25
GC	8.9	TC	8.2
GG	7.2	TG	14.6
GT	10.9	TT	7.6

A minimum value is used when N characters is present in a dinucleotide:

- CN, NC, GN, NG, NN: 7.2
- AN, NA, TN, NT : 7.6

- [Configuring Dialog Settings](#)
- [Result Annotations](#)